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| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

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1 ATC TTTGTTTCTAGT TTACCTCAGG GCTATTATGA 33

34 AATGAAATGA GATAACCAAT GTGAAAGTCC TATAAACTGT ATAGCCTCCA TTCGGATGTA 93

94 TGTCTTTGGC AGGATGATAA AGAATCAGGA AGAAGGAGTA TCCACGTTAG CCAAGTGTCC 153

154 AGGCTGTGTC TGCTCTTATT TTAGTGACAG ATGTTGCTCC TGACAGAAGC TATTCTTCAG 213

214 GAAACATCAC ATCCAATATG GTAAATCCAT CAAACAGGAG CTAAGAAACA GGAATGAGAT 273

274 GGGCACTTGC CCAAGGAAAA ATGCCAGGAG AGCAAATAAT GATGAAAAAT AAACCTTTTCC 333

334 CTTTGTTTTT AATTTTCAGGA AAAATGATG AGGACCAAAA TCAATGAATA AGGAAAAACAG 393
(Pr1.FPIII) CCTG AAAATGAATA AGAAA

394 CTCAGAAAAA AGATGTTTCC AAATTGGTAA TTAAGTATTT GTTCCTTGGG AAGAGACCTC 453
(PR/GR-MMTV) T GTTCTTTTGG AA
(SSRE) GAGACC

454 CATGTGAGCT TGATGGGAAA ATGGGAAAAA CGTCAAAAGC ATGATCTGAT CAGATCCCAA 513

514 AGTGGATTAT TATTTTAAAA ACCAGATGGC ATCACTCTGG GGAGGCAAGT TCAGGAAGGT 573

574 CATGTTAGCA AAGGACATAA CAATAACAGC AAAATCAAAA TTCCGCAAAT GCAGGAGGAA 633
CCTTTTAG-A AAGGACAAAA CAGAATG (nGRE-PRL)

634 AATGGGGACT GGGAAAGCTT TCATAACAGT GATTAGGCAG TTGACCATGT TCGCAACACC 693

694 TCCCCGTCTA TACCAGGGAA CACAAAAATT GACTGGGCTA AGCCTGGACT TTCAAGGGAA 753
GCCTGGACT GTC (CBE-P53)

754 ATATGAAAAA CTGAGAGCAA AACAAAAGAC ATGGTTAAAA GGCAACCAGA ACATTGTGAG 813
ATTTTCTGA TTGGTTAAAA GT (NFE1)

814 CCTTCAAAGC AGCAGTGCCC CTCAGCAGGG ACCCTGAGGC ATTTGCCTTT AGGAAGGCCA 873
G ACCCTGAGGC T (KTF.1-CS)

874 GTTTTCTTAA GGAATCTTAA GAAACTCTTG AAAGATCATG AATTTTAACC ATTTTAAGTA 933

934 TAAAACAAAT ATGCGATGCA TAATCAGTTT AGACATGGGT CCCAATTTTA TAAAGTCAGG 993
(PRE-lysozyme) AGGCCGT

994 CATACAAGGA TAACGTGTCC CAGCTCCGGA TAGGTCAGAA ATCATTAGAA ATCACTGTGT 1053
GATCCAAGGA GCAGAAGTTC CAGCTATGGT CAG (GRE-hMT) GG TCACTGTGT

1054 CCCCATCCTA ACTTTTTCAG AATGATCTGT CATAGCCCTC ACACACAGGC CCGATGTGTC 1113
CCT

1114 TGACCTACAA CCACATCTAC AACCCAAGTG CCTCAACCAT TGTTAACGTG TCATCTCAGT 1173

FIG. 1A

| | | |
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| APPROVED | O.G. FIG. | |
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1174 AGGTCCCATT ACAAATGCCA CCTCCCCTGT GCAGCCCATC CCGCTCCACA GGAAGTCTCC 1233

1234 CCACTCTAGA CTTCTGCATC ACGATGTTAC AGCCAGAAGC TCCGTGAGGG TGAGGGTCTG 1293
(SSRE) GGTCTC

1294 TGTCTTACAC CTACCTGTAT GCTCTACACC TGAGCTCACT GCAACCTCTG CCTCCCAGGT 1353

1354 TCAAGCAATT CTCCTGTCTC AGCCTCCCGC GTAGCTGGGA CTACAGGCGC ACGCCCGGCT 1413
C AGCCCCCGC GCAGC (ETF, EGFR)

1414 AATTTTGTGA TTGTTAGTAG AGATGGGGTT TCACCATATT AGCCCGGCTG GTCTTGAAGT 1473
Alu Repeat Region CCATATT AGG (SRE-cFos)

1474 CCTGACCTCA GGTGATCCAC CCACCTCAGC CTCCTAAAGT GCTGGGATTA CAGGCATGAG 1533

1534 TCACCGCGCC CGGCCAAGGG TCAGTGTTTA ATAAGGAATA ACTTGAATGG TTTACTAAAC 1593

1594 CAACAGGGAA ACAGACAAAA GCTGTGATAA TTTCAGGGAT TCTTGGGATG GGAATGGTG 1653

1654 CCATGAGCTG CCTGCCTAGT CCCAGACCAC TGGTCCTCAT CACTTTCTTC CCTCATCCTC 1713

1714 ATTTTCAGGC TAAGTTACCA TTTTATTCAC CATGCTTTTG TGTAAGCCT CCACATCGTT 1773

1774 ACTGAAATAA GAGTATACAT AACTAGTTC CATTTGGGGC CATCTGTGTG TGTGTATAGG 1833
GTTTACAT AAC (VBP-vitel) GG

1834 GGAGGAGGGC ATACCCAGAG GACTCCTTGA AGCCCCGGC AGAGGTTTCC TCTCCAGCTG 1893
GGAKGAGG (MaIT-CS)

1894 GGGGAGCCCT GCAAGCACCC GGGGTCTTGG GTGTCCTGAG CAACCTGCCA GCCCGTGCCA 1953

1954 CTGGTTGTTT TGTTATCACT CTCTAGGGAC CTGTTGCTTT CTATTTCTGT GTGACTCGTT 2013

2014 CATTATCCA GGCATTCAAT GACAATTTAT TGAGTACTTA TATCTGCCAG ACACCAGAGA 2073

2074 CAAAATGGTG AGCAAAGCAG TCACTGCCCT ACCTTCGTGG AGGTGACAGT TTCTCATGGA 2133

2134 AGACGTGCAG AAGAAAATTA ATAGCCAGCC AACTTAAACC CAGTGCTGAA AGAAAGGAAA 2193
GCGTGAC CGGAGCTGAA AGAAAGGAAC

2194 TAAACACCAT CTTGAAGAAT TGTGCGCAGC ATCCCTTAAC AAGGCCACCT CCCTAGCGCC 2253
AC (ERE-c.vitel)

2254 CCCTGCTGCC TCCATCGTGC CCGGAGGCC CCAAGCCGA GTCTTCCAAG CCTCCTCCTC 2313

2314 CATCAGTCAC AGCGCTGCAG CTGGCCTGCC TCGCTTCCcG TGAATCGTCC TGGTGCATCT 2373
AGCAG CTGGC (NF-mutagen)

2374 GAGCTGGAGA CTCCTTGGCT CCAGGCTCCA GAAAGGAAAT GGAGAGGGAA ACTAGTCTAA 2433
A GAAAGGGAAA GGA (PRF-myc)

2434 CGGAGAATCT GGAGGGGACA GTGTTTCCTC AGAGGGAAAG GGGCCTCCAC GTCCAGGAGA 2493
ACCCGGTACA CTGTGTCCTC CCGCT (GRE-hMT.IIa)
CC CTTTGGGCCA ATGTGTCCTG AGGGGA (GRE-hGH)

FIG.1B

| | | |
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| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
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2494 ATTCCAGGAG GTGGGGACTG CAGGGAGTGG GGACGCTGGG GCTGAGCGGG TGCTGAAAGG 2553
CTGG GGAGCCTGGG GA (AP.2-SV40)

2554 CAGGAAGGTG AAAAGGGCAA GGCTGAAGCT GCCCAGATGT TCAGTGTGTG TCACGGGGCT 2613

2614 GGGAGTTTTC CGTTGCTTCC TGTGAGCCTT TTTATCTTTT CTCTGCTTGG AGGAGAAGAA 2673
CT CGTTGCTTCG AG (HSTF-hsp70)

2674 GTCTATTTC A TGAAGGGATG CAGTTTCATA AAGTCAGCTG TTA^AAATTCC AGGGTGTGCA 2733

2734 TGGGTTTTCC TTCACGAAGG CCTTTATTTA ATGGGAATAT AGGAAGCGAG CTCATTTCTT 2793
TGGGTTTTTG (SBF yeast)

2794 AGGCCGTTAA TTCACGGAAG AAGTGA CTGG AGTCTTTTCT TTCATGTCTT CTGGGCAACT 2853

2854 ACTCAGCCCT GTGGTGGACT TGGCTTATGC AAGACGGTCG AAAACCTTGG AATCAGGAGA 2913

2914 CTCGGTTTTCT TTTCTGGTTC TGCCATTGGT TGGCTGTGCG ACCGTGGGCA AGTGTCTCTC 2973
C TTTCTGGTTT TGCAG (NF-1-bithorax)
(NF-MHCII/CCATTGGT T

2974 CTTCCCTGGG CCATAGTCTT CTCTGCTATA AAGACCCTTG CAGCTCTCGT GTTCTGTGAA 3033

3034 CACTTCCCTG TGATTCTCTG TGAGGGGGGA TGTGAGAGG GGAAGGAGGC AGAGCTGGAG 3093

3094 CAGCTGAGCC ACAGGGGAGG TGGAGGGGGA CAGGAAGCCA GGCAGAAGCT GGGTGCTCCA 3153

3154 TCAGTCCTCA CTGATCACGT CAGACTCCAG GACCGAGAGC CACAATGCTT CAGGAAAGCT 2943

2944 CAATGAACCC AACAGCCACA TTTTCCTTCC CTAAGCATAG ACAATGGCAT TTGCCAATAA 3273

3274 CCAAAAAGAA TGCAGAGACT AACTGGTGGT AGCTTTTGCC TGGCATTCAA AAAGTGGGCC 3333
GAAGTGACT AACTG (PEA.1-Polyoma)

3334 AGAGCAAGTG GAAAATGCCA GAGATTGTTA AACTTTTCAC CCGACCAGC ACCCCACGCA 3393

3394 GCTCAGCAGT GACTGCTGAC AGCACGGAGT GACCTGCAGC GCAGGGGAGG AGAAGAAAAA 3453
C AGGTCAGAGT GACCTG (ERE.2-Vitel.)

3454 GAGAGGGATA GTGTATGAGC AAGAAAGACA GATTCATTCA AGGGCAGTGG GAATTGACCA 3513

3514 CAGGGATTAT AGTCCACGTG ATCCTGGGTT CTAGGAGGCA GGGCTATATT GTGGGGGGAA 3573
(GRE-FLV) CGGGATAC CGAGAGAACA GGGCTATAGG

3574 AAAATCAGTT CAAGGGAAGT CGGGAGACCT GATTTC TAAT ACTATATTTT TCCTTTACAA 3633
GAGACC (SSRE)

3634 GCTGAGTAAT TCTGAGCAAG TCACAAGGTA GTAAGTGGG CTGTAAGATT ACTTAGTTTC 3693
(ICS-MTII/ HLA-DR/)AGTTTC

3694 TCCTTATTAG GAACTCTTTT TCTCTGTGGA GTTAGCAGCA CAAGGGCAAT CCCGTTTCTT 3753
TCCTCT

3754 TTAACAGGAA GAAACATTC CTAAGAGTAA AGCCAAACAG ATTCAAGCCT AGGTCTTGCT 3813

3814 GACTATATGA TTGGTTTTT GAAAAATCAT TTCAGCGATG TTTACTATCT GATTCAGAAA 3873

FIG. 1C

SECRET

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| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
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|------|------------|------------|------------|------------|------------|------------|------|
| 1474 | CCTGACCTCA | GGTGATCCAC | CCACCTCAGC | CTCCTAAAGT | GCTGGGATTA | CAGGCATGAG | 1533 |
| 1534 | TCACCGCGCC | CGGCCAAGGG | TCAGTGTTTA | ATAAGGAATA | ACTTGAATGG | TTTACTAAAC | 1593 |
| 1594 | CAACAGGGAA | ACAGACAAAA | GCTGTGATAA | TTTCAGGGAT | TCTTGGGATG | GGGAATGGTG | 1653 |
| 1654 | CCATGAGCTG | CCTGCCTAGT | CCCAGACCAC | TGGTCCTCAT | CACTTTCTTC | CCTCATCCTC | 1713 |
| 1714 | ATTTTCAGGC | TAAGTTACCA | TTTTATTAC | CATGCTTTTG | TGGTAAGCCT | CCACATCGTT | 1773 |
| 1774 | ACTGAAATAA | GAGTATACAT | AAACTAGTTC | CATTTGGGGC | CATCTGTGTG | TGTGTATAGG | 1833 |
| 1834 | GGAGGAGGGC | ATACCCCAGA | GACTCCTTGA | AGCCCCGGC | AGAGGTTTCC | TCTCCAGCTG | 1893 |
| 1894 | GGGGAGCCCT | GCAAGCACCC | GGGGTCCTGG | GTGTCCTGAG | CAACCTGCCA | GCCCGTGCCA | 1953 |
| 1954 | CTGGTTGTTT | TGTTATCACT | CTCTAGGGAC | CTGTTGCTTT | CTATTTCTGT | GTGACTCGTT | 2013 |
| 2014 | CATTCATCCA | GGCATTCAAT | GACAATTTAT | TGAGTACTTA | TATCTGCCAG | ACACCAGAGA | 2073 |
| 2074 | CAAAATGGTG | AGCAAAGCAG | TCACTGCCCT | ACCTTCGTGG | AGGTGACAGT | TTCTCATGGA | 2133 |
| 2134 | AGACGTGCAG | AAGAAAATTA | ATAGCCAGCC | AACTTAAACC | CAGTGCTGAA | AGAAAGGAAA | 2193 |
| 2194 | TAAACACCAT | CTTGAAGAAT | TGTGCGCAGC | ATCCCTTAAC | AAGGCCACCT | CCCTAGCGCC | 2253 |
| 2254 | CCCTGCTGCC | TCCATCGTGC | CCGGAGGCCC | CCAAGCCCGA | GTCTTCCAAG | CCTCCTCCTC | 2313 |
| 2314 | CATCAGTCAC | AGCGCTGCAG | CTGGCCTGCC | TCGCTTCCCG | TGAATCGTCC | TGGTGCATCT | 2373 |
| 2374 | GAGCTGGAGA | CTCCTTGGCT | CCAGGCTCCA | GAAAGGAAAT | GGAGAGGGAA | ACTAGTCTAA | 2433 |
| 2434 | CGGAGAATCT | GGAGGGGACA | GTGTTTCCTC | AGAGGGAAAG | GGGCCTCCAC | GTCCAGGAGA | 2493 |
| 2494 | ATTCCAGGAG | GTGGGGACTG | CAGGGAGTGG | GGACGCTGGG | GCTGAGCGGG | TGCTGAAAGG | 2553 |
| 2554 | CAGGAAGGTG | AAAAGGGCAA | GGCTGAAGCT | GCCCAGATGT | TCAGTGTTGT | TCACGGGGCT | 2613 |
| 2614 | GGGAGTTTTC | CGTTGCTTCC | TGTGAGCCTT | TTTATCTTTT | CTCTGCTTGG | AGGAGAAGAA | 2673 |
| 2674 | GTCTATTTCA | TGAAGGGATG | CAGTTTCATA | AAGTCAGCTG | TTAAAATTCC | AGGGTGTGCA | 2733 |
| 2734 | TGGGTTTTTC | TTCACGAAGG | CCTTTATTTA | ATGGGAATAT | AGGAAGCGAG | CTCATTTCTT | 2793 |
| 2794 | AGGCCGTAA | TTCACGGAAG | AAGTGACTGG | AGTCTTTTCT | TTCATGTCTT | CTGGGCAACT | 2853 |
| 2854 | ACTCAGCCCT | GTGGTGGAAT | TGGCTTATGC | AAGACGGTCG | AAAACCTTGG | AATCAGGAGA | 2913 |
| 2914 | CTCGGTTTTT | TTTCTGGTTC | TGCCATTGGT | TGGCTGTGCG | ACCGTGGGCA | AGTGTCTCTC | 2973 |
| 2974 | CTTCCCTGGG | CCATAGTCTT | CTCTGCTATA | AAGACCCTTG | CAGCTCTCGT | GTTCTGTGAA | 3033 |
| 3034 | CACTTCCCTG | TGATTCTCTG | TGAGGGGGGA | TGTTGAGAGG | GGAAGGAGGC | AGAGCTGGAG | 3093 |

FIG. 2B

| | | |
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| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
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3094 CAGCTGAGCC ACAGGGGAGG TGGAGGGGGA CAGGAAGGCA GGCAGAAGCT GGGTGCTCCA 3153
3154 TCAGTCCTCA CTGATCACGT CAGACTCCAG GACCGAGAGC CACAATGCTT CAGGAAAGCT 2943
2944 CAATGAACCC AACAGCCCACA TTTTCCTTCC CTAAGCATAG ACAATGGCAT TTGCCAATAA 3273
3274 CCAAAAAGAA TGCAGAGACT AACTGGTGGT AGCTTTTGCC TGGCATTCAA AAAGTGGGCC 3333
3334 AGAGCAAGTG GAAAATGCCA GAGATTGTGA AACTTTTCAC CCTGACCAGC ACCCCACGCA 3393
3394 GCTCAGCAGT GACTGCTGAC AGCACGGAGT GACCTGCAGC GCAGGGGAGG AGAAGAAAAA 3453
3454 GAGAGGGATA GTGTATGAGC AAGAAAGACA GATTCATTCA AGGGCAGTGG GAATTGACCA 3513
3514 CAGGGATTAT AGTCCACGTG ATCCTGGGTT CTAGGAGGCA GGGCTATATT GTGGGGGGAA 3573
3574 AAAATCAGTT CAAGGGAAGT CGGGAGACCT GATTTCTAAT ACTATATTTT TCCTTTACAA 3633
3634 GCTGAGTAAT TCTGAGCAAG TCACAAGGTA GTAAGTGGG CTGTAAGATT ACTTAGTTTC 3693
3694 TCCTTATTAG GAACTCTTTT TCTCTGTGGA GTTAGCAGCA CAAGGGCAAT CCCGTTTCTT 3753
3754 TTAACAGGAA GAAAACATTC CTAAGAGTAA AGCCAAACAG ATTCAAGCCT AGGTCTTGCT 3813
3814 GACTATATGA TTGGTTTTTT GAAAAATCAT TTCAGCGATG TTTACTATCT GATTGAGAAA 3873
3874 ATGAGACTAG TACCTTTTGG TCAGCTGTAA ACAAACACCC ATTTGTAAAT GTCTCAAGTT 3933
3934 CAGGCTTAAC TGCAGAACCA ATCAAATAAG AATAGAATCT TTAGAGCAAA CTGTGTTTCT 3993
3994 CCACTCTGGA GGTGAGTCTG CCAGGGCAGT TTGGAAATAT TTAAGTTCACA AGTATTGACA 4053
4054 CTGTTGTTGG TATTAACAAC ATAAAGTTGC TCAAAGGCAA TCATTATTTC AAGTGGCTTA 4113
4114 AAGTTACTTC TGACAGTTTT GGTATATTTA TTGGCTATTG CCATTGCTT TTTGTTTTTT 4173
4174 CTCTTTGGGT TTATTAATGT AAAGCAGGGA TTATTAACCT ACAGTCCAGA AAGCCTGTGA 4233
4234 ATTTGAATGA GGAAAAAATT ACGTTTTTAT TTTTACCACC TTCTAACTAA ATTTAACATT 4293
4294 TTATTCCATT GCGAATAGAG CCATAAACTC AAAGTGGTAA TAAGAGTACC TGTGATTTTG 4353
4354 TCATTACCAA TAGAAATCAC AGACATTTTA TACTATATTA CAGTTGTTGC AGGTACGTTG 4413
4414 TAAGTGAAAT ATTTATACTC AAACTACTT TGAAATTAGA CCTCCTGCTG GATCTTGTTT 4473
4474 TTAACATATT AATAAAACAT GTTTAAAATT TTGATATTTT GATAATCATA TTTCATTATC 4533
4534 ATTTGTTTCC TTTGTAATCT ATATTTTATA TATTTGAAAA CATCTTCTG AGAAGAGTTC 4593
4594 CCCAGATTTT ACCAATGAGG TTCTTGGCAT GCACACACAC AGAGTAAGAA CTGATTTAGA 4653
4654 GGCTAACATT GACATTGGTG CCTGAGATGC AAGACTGAAA TTAGAAAGTT CTCCCAAAGA 4713

FIG.2C

00227004 01109

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| APPROVED | O.G. FIG. | |
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4714 TACACAGTTG TTTTAAAGCT AGGGGTGAGG GGGGAAATCT GCCGCTTCTA TAGGAATGCT 4773
4774 CTCCCTGGAG CCTGGTAGGG TGCTGTCCTT GTGTTCTGGC TGGCTGTTAT TTTTCTCTGT 4833
4834 CCCTGCTACG TCTTAAAGGA CTTGTTTGGA TCTCCAGTTC CTAGCATAGT GCCTGGCACA 4893
4894 GTGCAGGTTC TCAATGAGTT TGCAGAGTGA ATGGAAATAT AACTAGAAA TATATCTTTG 4953
4954 TTGAAATCAG CACACCAGTA GTCCTGGTGT AAGTGTGTGT ACGTGTGTGTGTGT GTGTGTGTGT5017
5018 GTGTGTGTGT AAAACCAGGT GGAGATATAG GAACTATTAT TGGGGTATGG GTGCATAAAT 5077
5078 TGGGATGTTT TTTTAAAAA GAACTCCAA ACAGACTTCT GGAAGGTTAT TTTCTAAGAA 5137
5138 TCTTGCTGGC AGCGTGAAGG CAACCCCCCT GTGCACAGCC CCACCCAGCC TCACGTGGCC 5197
5198 ACCTCTGTCT TCCCCATGA AGGGCTGGCT CCCAGTATA TATAAACCTC TCTGGAGCTC 5257
5258 GGGCATGAGC CAGCAAGGCC ACCCATCCAG GCACCTCTCA GCACAGC 5304

0027591 04499

FIG.2D

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| APPROVED | O.G. FIG. | |
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1 ATCTTTGTTT AGTTTACCTC AGGGCTATTA TGAAATGAAA TGAGATAACC
 51 AATGTGAAAG TCCTATAAAC TGTATAGCCT CCATTCCGGAT GTATGTCTTT
 101 GGCAGGATGA TAAAGAATCA GGAAGAAGGA GTATCCACGT TAGCCAAGTG
 151 TCCAGGCTGT GTCTGCTCTT ATTTTAGTGA CAGATGTTGC TCCTGACAGA
 201 AGCTATTCTT CAGGAAACAT CACATCCAAT ATGGTAAATC CATCAAACAG
 251 GAGCTAAGAA ACAGGAATGA GATGGGCACT TGCCCAAGGA AAAATGCCAG
 301 GAGAGCAAAT AATGATGAAA AATAAACTTT TCCCTTTGTT TTTAATTTCA
 351 GGAAAAAATG ATGAGGACCA AAATCAATGA ATAAGGAAAA CAGCTCAGAA
 401 AAAAGATGTT TCCAAATTGG TAATTAAGTA TTTGTTCTT GGAAGAGAC
 451 CTCCATGTGA GCTTGATGGG AAAATGGGAA AAACGTCAAA AGCATGATCT
 501 GATCAGATCC CAAAGTGGAT TATTATTTTA AAAACCAGAT GGCATCACTC
 551 TGGGGAGGCA AGTTCAGGAA GGTGATGTTA GCAAAGGACA TAACAATAAC
 601 AGCAAAATCA AAATTCCGCA AATGCAGGAG GAAAATGGGG ACTGGGAAAG
 651 CTTTCATAAC AGTGATTAGG CAGTTGACCA TGTCGCAAC ACCTCCCCGT
 701 CTATACCAGG GAACACAAAA ATTGACTGGG CTAAGCCTGG ACTTTCAAGG
 751 GAAATATGAA AACTGAGAG CAAAACAAAA GACATGGTTA AAAGGCAACC
 801 AGAACATTGT GAGCCTTCAA AGCAGCAGTG CCCCTCAGCA GGGACCCTGA
 851 GGCATTTGCC TTTAGGAAGG CCAGTTTTCT TAAGGAATCT TAAGAACTC
 901 TTGAAAGATC ATGAATTTTA ACCATTTTAA GTATAAAACA AATATGCGAT
 951 GCATAATCAG TTTAGACATG GGTCCCAATT TTATAAAGTC AGGCATACAA
 1001 GGATAACGTG TCCCAGCTCC GGATAGGTCA GAAATCATT AATCACTG
 1051 TGTCCCCATC CTAACTTTTT CAGAATGATC TGTCATAGCC CTCACACACA
 1101 GGCCCGATGT GTCTGACCTA CAACCACATC TACAACCCAA GTGCCTCAAC
 1151 CATTGTTAAC GTGTCATCTC AGTAGGTCCC ATTACAAATG CCACCTCCCC
 1201 TGTGCAGCCC ATCCCGCTCC ACAGGAAGTC TCCCCTCT AGACTTCTGC
 1251 ATCACGATGT TACAGCCAGA AGCTCCGTGA GGGTGAGGGT CTGTGTCTTA

00227594 01199

FIG.3A

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| APPROVED | O.G. FIG. | |
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4001 GGAGGTGAGT CTGCCAGGGC AGTTTGAAAA TATTTACTTC ACAAGTATTG
4051 AACTGTTGT TGGTATTAAC AACATAAAGT TGCTCAAAGG CAATCATTAT
4101 TTCAAGTGGC TTAAAGTTAC TTCTGACAGT TTTGGTATAT TTATTGGCTA
4151 TTGCCATTTG CTTTTTGTTT TTTCTCTTTG GGTTTATTAA TGTAAGCAG
4201 GGATTATTAA CCTACAGTCC AGAAAGCCTG TGAATTTGAA TGAGGAAAAA
4251 ATTACATTTT TGTTTTTACC ACCTTCTAAC TAAATTTAAC ATTTTATTCC
4301 ATTGCGAATA GAGCCATAAA CTCAAAAGTG TAATAACAGT ACCTGTGATT
4351 TTGTCATTAC CAATAGAAAT CACAGACATT TTATACTATA TTACAGTTGT
4401 TGCAGATACG TTGTAAGTGA AATATTTATA CTCAAAATA CTTTGAAATT
4451 AGACCTCCTG CTGGATCTTG TTTTAAACAT ATTAATAAAA CATGTTTAAA
4501 ATTTTGATAT TTTGATAATC ATATTTCAAT ATCATTTGTT TCCTTTGTAA
4551 TCTATATTTT ATATATTTGA AAACATCTTT CTGAGAAGAG TTCCCCAGAT
4601 TTCACCAATG AGGTTCTTGG CATGCACACA CACAGAGTAA GAACTGATTT
4651 AGAGGCTAAC ATTGACATTG GTGCCTGAGA TGCAAGACTG AAATTAGAAA
4701 GTTCTCCCAA AGATACACAG TTGTTTTAAA GCTAGGGGTG AGGGGGGAAA
4751 TCTGCCGCTT CTATAGGAAT GCTCTCCCTG GAGCCTGGTA GGGTGCTGTC
4801 CTTGTGTTCT GGCTGGCTGT TATTTTCTC TGTCCCTGCT ACGTCTTAAA
4851 GGACTTGTTT GGATCTCCAG TTCCTAGCAT AGTGCCTGGC ACAGTGCAGG
4901 TTCTCAATGA GTTTGCAGAG TGAATGAAAA TATAAACTAG AAATATATCC
4951 TTGTTGAAAT CAGCACACCA GTAGTCCTGG TGTAAGTGTG TGTACGTGTG
5001 TGTGTGTGTG TGTGTGTGTG TGTA AAAACCA GGTGGAGATA TAGGAACTAT
5051 TATTGGGGTA TGGGTGCATA AATTGGGATG TTCTTTTTTAA AAAGAACTC
5101 CAAACAGACT TCTGGAAGGT TATTTTCTAA GAATCTTGCT GGCAGCGTGA
5151 AGGCAACCCC CCTGTGCACA GCCCCACCCA GCCTCACGTG GCCACCTCTG
5201 TCTTCCCCCA TGAAGGGCTG GCTCCCCAGT ATATATAAAC CTCTCTGGAG
5251 CTCGGGCATG AGCCAGCAAG GCCACCCATC CAGGCACCTC TCAGCACAGC 5300

FIG. 3D

| | | |
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| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

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1 AGAGCTTTCCAGAGGAAGCCTCACCAAGCCTCTGCAATGAGGTTCTTCTGTGCACGTTGC 60
61 TGCAGCTTTGGGCTGAGATGCCAGCTGTCCAGCTGCTGCTTCTGGCCTGCCTGGTGTGG 120
121 GATGTGGGGGCCAGGACAGCTCAGCTCAGGAAGGCCAATGACCAGAGTGGCCGATGCCAG 180
181 TATACCTTCAGTGTGGCCAGTCCCAATGAATCCAGCTGCCCAGAGCAGAGCCAGGCCATG 240
241 TCAGTCATCCATAACTTACAGAGAGACAGCAGCACCCAACGCTTAGACCTGGAGGCCACC 300
301 AAAGCTCGACTCAGCTCCCTGGAGAGCCTCCTCCACCAATTGACCTTGGACCAGGCTGCC 360
361 AGGCCCCAGGAGACCCAGGAGGGGCTGCAGAGGGAGCTGGGCACCCTGAGGCGGGAGCGG 420
421 GACCAGCTGGAAACCCAAACCAGAGAGTTGGAGACTGCCTACAGCAACCTCCTCCGAGAC 480
481 AAGTCAGTTCTGGAGGAAGAGAAGAAGCGACTAAGGCAAGAAAATGAGAATCTGGCCAGG 540
541 AGGTTGGAAGCAGCAGCCAGGAGGTAGCAAGGCTGAGAAGGGGCCAGTGTCCCAGACC 600
601 CGAGACACTGCTCGGGCTGTGCCACCAGGCTCCAGAGAAG

(intron #1) gtaagaatgcagagtggggggactct
gagttcagcaggtgatatggctcgtagtgacctgctacaggcgctccaggccctccctgccctttctccta
gagactgcacagctagcacagacagatgaattaaggaaagcacacgatcaccttcaagtattacta
gtaatttagctcctgagagcttcatttagattagtggttcagagttcttgtgccctccatgtcag-----
----- Intron I ~10 Kb-----
aaggtaggcacattgccctgcaatttataatttatgaggtgttcaattatggaattgtcaaataattaaca
aaagtagagagactacaatgaactccaatgtagccataactcaggcccaactgttatcagcacagtcc
aatcatgttttatctttcttctctgacccccaacccatccccagtccttatctaaaaatcaaatatcaaaca
ccatactctttgggagcctatttatttagtttagttttcagacagagtttctttcttgttcccaagctgg
agtacaatagtgtagtctcggtacacagcaatctcccctccttggttcaagcaattctectgcctcagtc
tcccaagaagctgggattatagacacctgcaccaccatccagctaattttttgtgttttagaaaagaca
gggtttccacctgttggccaggctgggttcgaactctgtacctcaggtgatccgctgcctcggcctccca
aagtgctgggattacagggcatgagccaccacgcctggccggcagcctattttaattgtcctcctcaacat
agtcaatccttgggccatttttcttacagtaaaattttgtctctttcttttaatacag

(exon #2) TT TCT ACG TGG AAT TTG GAC

661 ACT TTG GCC TTC CAG GAACTG AAG TCC GAG CTA ACT GAAGTT CCT GCT TCC CGA ATT TTG 720
721 AAG GAG AGC CCA TCT GGC TAT CTC AGG AGT GGA GAG GGA GAC ACCG

(intron #2)
gtatgaagttaagtttcttcccttttggtgccacgtggtctttattcatgtctagtgtgtgttcagagaa
tcagtatagggtaaatgccacccaaggggaaattaacttccctgggagcagaagggagggagga
gaagaggaacagaactctctctctctctgttacccttg-----Intron II ~ 3 kb-----

FIG. 3E

| | | |
|-----------|-----------|----------|
| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

15/23

66770-7382200

tggtctgtccaaagcttccgcgatgattctgtgtgtttggaagattatggattaagtgtgcttcgtttt
ctttctgaattaccag

(exon #3) GA TGT GGA GAA CTA 780

781 GTT TGG GTA GGA GAG CCT CTC ACG CTG AGA ACA GCA GAA ACA ATT ACT GGC AAG TAT GGT 840
841 GTG TGG ATG CGA GAC CCC AAG CCT AAG CCC ACC TAC CCC TAC ACC CAG GAG ACC ACG TGG AGA ATC 900
901 GAC ACA GTT GGC ACG GAT GTC CGC CAG GTT TTT GAG TAT GAC CTC ATC AGC CAG TTT ATG 960
961 CAG GGC TAC CCT TCT AAG GTT CAC ATA CTG CCT AGG CCA CTG GAA AGC ACG GGT GCT GTG 1020
1021 GTG TAC TCG GGG AGC CTC TAT TTC CAG GGC GCT GAG TCC AGA ACT GTC ATA AGA TAT GAG 1080
1081 CTG AAT ACC GAG ACA GTG AAG GCT GAG AAG GAA ATC CCT GGA GCT GGC TAC CAC GGA CAG 1140
1141 TTC CCG TAT TCT TGG GGT GGC TAC ACG GAC ATT GAC TTG GCT GTG GAT GAA GCA GGC CTC 1200
1201 TGG GTC ATT TAC AGC ACC GAT GAG GCC AAA GGT GCC ATT GTC CTC TCC AAA CTG AAC CCA 1260
1261 GAG AAT CTG GAA CTC GAA CAA ACC TGG GAG ACA AAC ATC CGT AAG CAG TCA GTC GCC AAT 1320
1321 GCC TTC ATC ATC TGT GGC ACC TTG TAC ACC GTC AGC AGC TAC ACC TCA GCA GAT GCT ACC 1380
1381 GTC AAC TTT GCT TAT GAC ACA GGC ACA GGT ATC AGC AAG ACC CTG ACC ATC CCA TTC AAG 1440
1441 AAC CGC TAT AAG TAC AGC AGC ATG ATT GAC TAC AAC CCC CTG GAG AAG AAG CTC TTT GCC 1500
1501 TGG GAC AAC TTG AAC ATG GTC ACT TAT GAC ATC AAG CTC TCC AAG ATG

(3' flanking region) TGA AAA GCC TCC 1560

1561 AAG CTG TAC AGG CAA TGG CAG AAG GAG ATG CTC AGG GCT CCT GGG GGG AGC AGG CTG AAG 1620
1621 GGA GAG CCA GCC AGC CAG GGC CCA ACC ATC TAA CTA TTC AGG AAT TGT CCA AGT TTT CAT TAA TCC 1680
1681 AGA AGG ATG AAC ATG GTC ACC ATC TAA CTA TTC AGG AAT TGT CCA AGT TTT CAT TAA TCC 1740
1741 ATT TCA TAT AAT AAA TAT CCT TTA TCT TCT GTC AGC ATT TAT GGG ATG TTT AAT GAC ATA 1800
1801 GTT CAA GTT TTC TTT TGA TGT TGA TTT GGG GCA AAA GCT GTA AGG CAT AAT AGT CTC CTG AAA 1860
1861 ACC ATT GCT CTT GCA TGT TAC ATG GTT ACC ACA AGC CAC AAT AAA AAG CAT AAC TTC TAA 1920
1921 AGG AAG CAG AAT AGC TCC TCT GGC CAG CAT CGA ATA TAA GTA AGA TGC ATT TAC TAC AGT 1980
1981 TGG CTT CTA ATG CTT CAG ATA GAA TAC AGT TGG GTC TCA CAT AAC CCT TAC ATT GTG AAA 2040
2041 TAA AAT TTT CTT ACC CAA CGT TCT CTT CTT TGA ACT TTG TGG GAA TCT TTG CTT AAG AGA 2100
2101 AGG ATA TAG ATT CCA ACC ATC AGG TAA TTC CTT CAG GTT GGG AGA TGT GAT TGC AGG ATG 2160

FIG.3F

2161 TTA AAG GTG TGT GTG TGT GTG TGT GTG TAA CTG AGA GGC TTG TGC CTG GTT TTG 2220

2221 AGG TGC TGC CCA GGA TGA CGC CAA GCA AAT AGC GCA TCC ACA CTT TCC CAC CTC CAT CTC 2280

2281 CTG GTG CTC TCG GCA CTA CCG GAG CAA TCT TTC CAT CTC TCC CCT GAA CCC ACC CTC TAT 2340

2341 TCA CCC TAA CTC CAC TTC AGT TTG CTT TTG ATT TTT TTT TTT TTT TTT TGA 2400

2401 GAT GGG GTC TCG CTC TGT CAC CCA GGC TGG AGT GCA GTG GCA CGA TCT CGG CTC ACT GCA 2460

2461 AGT TCC GCC TCC CAG GTT CAC ACC ATT CTC CTG CCT CAG CCT CCC AAG TAG CTG GGA CTA 2520

2521 CAG GCA CCT GCC ACC ACG CCT GGC TAA TTT TTT TTT TTT CCA GTG AAG ATG GGT TTC ACC 2580

2581 ATG TTA GCC AGG ATG GTC TCG ATC TCC TGAC CTT GTC ATC CAC CCA CCT TGG CCT CCC AAA 2640

2641 GTG CTG GGA TTA CAG GCG TGA GCC ACC ACGC CCA GCC CCT CCA CTT CAG TTT TTA TCT GTC 2700

2701 ATC AGG GGT ATG AAT TTT ATA AGC CAC ACC TCA GGT GGA GAA AGC TTG ATG CAT AGC TTG 2760

2761 AGT ATT CTA TAC TGT 2776

FIG. 3G

| | | |
|-----------|-----------|----------|
| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

17/23

05710-1332200

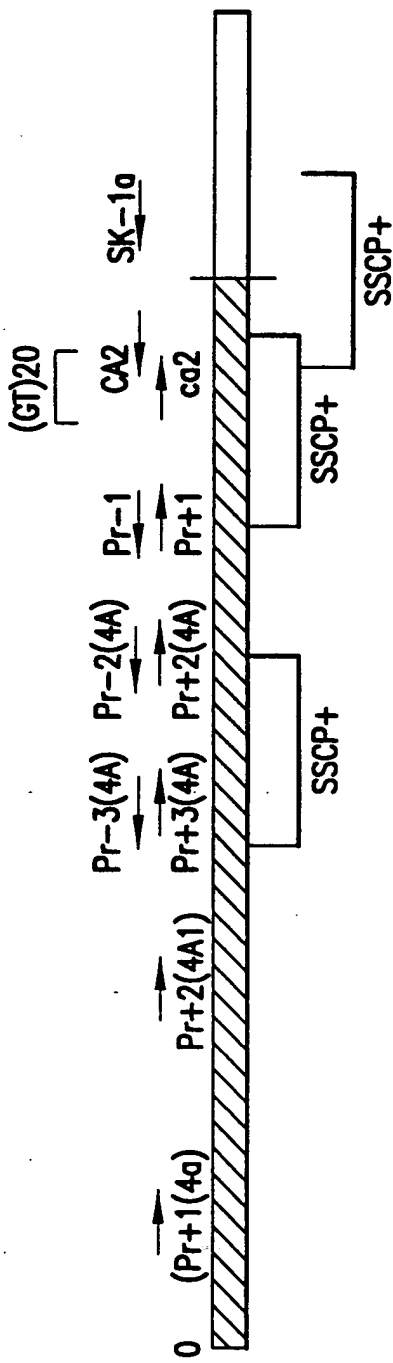


FIG.4

| | | |
|-----------|-----------|----------|
| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

18/23

05TFO: T882200

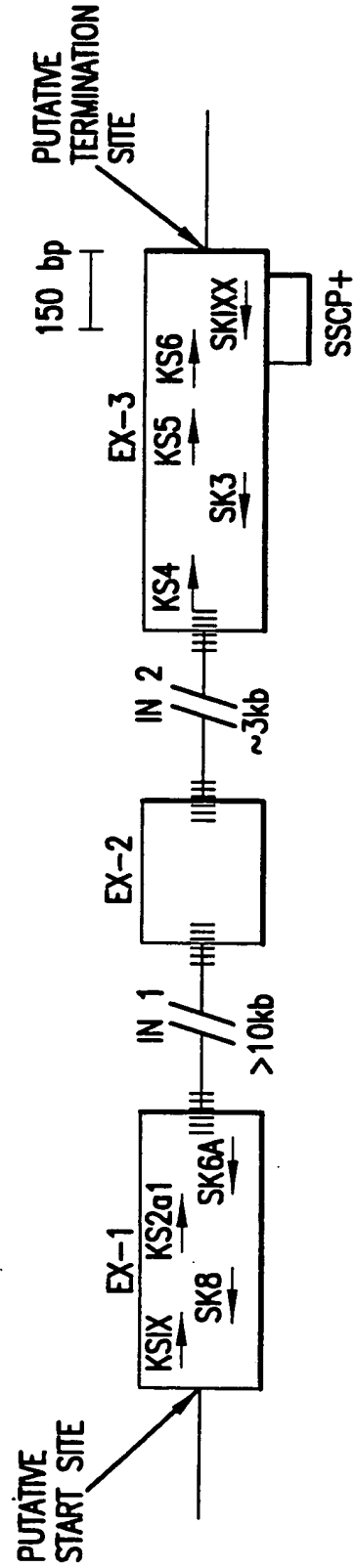


FIG.5

| | | |
|-----------|-----------|----------|
| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

SECRET

19/23

| | TIGR | ym08h12.r1 | 18426bamZ | ranofm | Consensus |
|------------|------------|------------|------------|------------|------------|
| -TGAVVSGS | LYFQGAESRT | VIRYELNTET | VKAKEIPGA | GYHGQFPYSW | GGYTDIDLAV |
| ----- | ----- | --RFDLKTET | ILKTRSLDYA | GYNNMYHYAW | GGHSDIDLNV |
| GTGQVVYNGS | IYFNKFQSHI | IIRFDLKTET | ILKTRSLDYA | GYNNMYHYAW | GGHSDIDLNV |
| GAGVVVHNNN | LYYNCFNSHD | MCRASL-TSG | VYQKKPLLNA | LFNNRFSYAG | TMFQDMDFSS |
| .G.VV.... | .Y....S... | .R..L..TET |L...A | GYNN...YAW | GG..DIDL.V |

| TIGR | DEAGLWVIYS | TDEAKGAIVL | SKLNPENLEL | EQTWETNIRK | QSVANAFIIC | GTLTYTVSSYT | 119 |
|------------|------------|------------|-------------|-------------|------------|-------------|-----|
| ym08h12.r1 | DESGLWAVYA | TNQAGNIIV | SRLDPVSLQT | LQTWNTSYPK | RXPGXAFIIC | GTCVVTNGY | 97 |
| 1B426bAMZ | DENGLWAVYA | TNQAGNIVI | SKLDPVSLQI | LQTWNTSYPK | RSAGEAFIIC | GTLTYVTNGYS | 120 |
| ranofm | DEKGLWVIFT | TEKSAGKIIV | GKVNVAFTIV | DNIIWITTQNK | SDASNAFMIC | GVLYVTRSLG | 119 |
| Consensus | DE.GLW..Y. | T...AG.IV. | SKL.P.L.L.. | .QTw.T...K |AFIIC | GTLTYT..Y. | 120 |

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
|------------|---------|-------|-------|--------|--------|-------|-------|-------|-------|-----|-----|-------|-------|--------|-------|-----|----|----|
| TIGR | SADATVN | FAY | DTGTG | ISKTL | TIPFK | NRVKY | SSMID | YNPLE | KKLFA | WDN | LN | MVTYD | IKLS | 178 | | | | |
| ym08h12.r1 | SGG | TKVHY | AY | QTNAST | --- | --- | Y | --- | IDI | - | PFQ | NKLXP | --- | --HFPC | 131 | | | |
| 1B426bAMZ | GG | - | TKVHY | AY | QTNAST | Y | Y | --- | ISML | DYN | PKD | RALYA | WNNGH | QTL | YNVT | 178 | | |
| ranofm | PKMEE | V | YMF | DTKTG | KEGHL | SIMME | KMAEK | VHSL | S | YNS | ND | RKL | YMF | SEGY | LLHYD | 177 | | |
| Consensus | | V | YAY | T | | I | | Y | | DYN | P | KL | | Y | | 178 | | |

FIG. 6

| | | |
|-----------|-----------|----------|
| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

21/23

667707 7332200

901 GAC ACA GTT GGC ACG GAT GTC CGC CAG GTT TTT GAG TAT GAC CTC ATC AGC CAG TTT ATG 960
 961 CAG GGC TAC CCT TCT AAG GTT CAC ATA CTG CCT AGG CCA CTG GAA AGC ACG GGT GCT GTG 1020
 1021 GTG TAC TCG GGG AGC CTC TAT TTC CAG GGC GCT GAG TCC AGA ACT GTC ATA AGA TAT GAG 1080
 1081 CTG AAT ACC GAG ACA GTG AAG GCT GAG AAG GAA ATC CCT GGA GCT GGC TAC CAC GGA CAG 1140
 1141 TTC CCG TAT TCT TGG GGT GGC TAC ACG GAC ATT GAC TTG GCT GTG GAT GAA GCA GGC CTC 1200
 1201 TGG GTC ATT TAC AGC ACC GAT GAG GCC AAA GGT GCC ATT GTC CTC TCC AAA CTG AAC CCA 1260
 1261 GAG AAT CTG GAA CTC GAA CAA ACC TGG GAG ACA AAC ATC CGT AAG CAG TCA GTC GCC AAT 1320
 1321 GCC TTC ATC ATC TGT GGC ACC TTG TAC ACC GTC AGC AGC TAC ACC TCA GCA GAT GCT ACC 1380
 1381 GTC AAC TTT GCT TAT GAC ACA GGC ACA GGT ATC AGC AAG ACC CTG ACC ATC CCA TTC AAG 1440
 1441 AAC CGC TAT AAG TAC AGC AGC ATG ATT GAC TAC AAC CCC CTG GAG AAG AAG CTC TTT GCC 1500
 1501 TGG GAC AAC TTG AAC ATG GTC ACT TAT GAC ATC AAG CTC TCC AAG ATG 1548

FIG.7B

| | | |
|-----------|-----------|----------|
| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

22/23

05F10-7882260

1 Met Arg Phe Phe Cys Ala Arg Cys 20

21 Cys Ser Phe Gly Pro Glu Met Pro Ala Val Gln Leu Leu Ala Cys Leu Val Trp 40

41 Asp Val Gly Ala Arg Thr Ala Gln Leu Arg Lys Ala Asn Asp Gln Ser Gly Arg Cys Gln 60

61 Tyr Thr Phe Ser Val Ala Ser Pro Asn Glu Ser Ser Cys Pro Glu Gln Ser Gln Ala Met 80

81 Ser Val Ile His Asn Leu Gln Arg Asp Ser Ser Thr Gln Arg Leu Asp Leu Glu Ala Thr 100

101 Lys Ala Arg Leu Ser Ser Leu Glu Ser Leu Leu His Gln Leu Thr Leu Asp Gln Ala Ala 120

121 Arg Pro Gln Glu Thr Gln Glu Gly Leu Gln Arg Glu Leu Gly Thr Leu Arg Arg Glu Arg 140

141 Asp Gln Leu Glu Thr Gln Thr Arg Glu Leu Glu Thr Ala Tyr Ser Asn Leu Leu Arg Asp 160

161 Lys Ser Val Leu Glu Glu Lys Lys Arg Leu Arg Gln Glu Asn Glu Asn Leu Ala Arg 180

181 Arg Leu Glu Ser Ser Gln Glu Val Ala Arg Leu Arg Arg Gly Gln Cys Pro Gln Thr 200

201 Arg Asp Thr Ala Arg Ala Val Pro Pro Gly Ser Arg Glu Val Ser Thr Trp Asn Leu Asp 220

221 Thr Leu Ala Phe Gln Glu Leu Lys Ser Glu Leu Thr Glu Val Pro Ala Ser Arg Ile Leu 240

241 Lys Glu Ser Pro Ser Gly Tyr Leu Arg Ser Gly Glu Gly Asp Thr Gly Cys Gly Glu Leu 260

261 Val Trp Val Gly Glu Pro Leu Thr Leu Arg Thr Ala Glu Thr Ile Thr Gly Lys Tyr Gly 280

281 Val Trp Met Arg Asp Pro Lys Pro Thr Tyr Pro Tyr Thr Gln Glu Thr Thr Trp Arg Ile 300

FIG.8A

| | | |
|-----------|-----------|----------|
| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

23/23

001110-18842260

301 Asp Thr Val Gly Thr Asp Val Arg Gln Val Phe Glu Tyr Asp Leu Ile Ser Gln Phe Met 320
 321 Gln Gly Tyr Pro Ser Lys Val His Ile Leu Pro Arg Pro Leu Glu Ser Thr Gly Ala Val 340
 341 Val Tyr Ser Gly Ser Leu Tyr Phe Gln Gly Ala Glu Ser Arg Thr Val Ile Arg Tyr Glu 360
 361 Leu Asn Thr Glu Thr Val Lys Ala Glu Lys Glu Ile Pro Gly Ala Gly Tyr His Gly Gln 380
 381 Phe Pro Tyr Ser Trp Gly Gly Tyr Thr Asp Ile Asp Leu Ala Val Asp Glu Ala Gly Leu 400
 401 Trp Val Ile Tyr Ser Thr Asp Glu Ala Lys Gly Ala Ile Val Leu Ser Lys Leu Asn Pro 420
 421 Glu Asn Leu Glu Leu Glu Gln Thr Trp Glu Thr Asn Ile Arg Lys Gln Ser Val Ala Asn 440
 441 Ala Phe Ile Ile Cys Gly Thr Leu Tyr Thr Val Ser Ser Tyr Thr Ser Ala Asp Ala Thr 460
 461 Val Asn Phe Ala Tyr Asp Thr Gly Thr Gly Ile Ser Lys Thr Leu Thr Ile Pro Phe Lys 480
 481 Asn Arg Tyr Lys Tyr Ser Ser Met Ile Asp Tyr Asn Pro Leu Glu Lys Lys Leu Phe Ala 500
 501 Trp Asp Asn Leu Asn Met Val Thr Tyr Asp Ile Lys Leu Ser Lys Met

FIG.8B